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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 11-1-05  
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 09/699,667  
Location (Bldg/Room#): 2D28 (Mailbox #): 2C12 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: NA enzyme  
Inventors (please provide full names): J-P Perreault et al.

Earliest Priority Date: 4-29-99

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID Nos:

62, 65, 66

- Limit to ~~200~~ 200 NTS
- No size limits
- Please include interference searches.

Thanks

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Type of Search		Vendors and cost where applicable
Searcher: _____	____ NA Sequence (#)	____ STN _____ Dialog
Searcher Phone #: _____	____ AA Sequence (#)	____ Questel/Orbit _____ Lexis/Nexis
Searcher Location: _____	____ Structure (#)	____ Westlaw _____ WWW/Internet
Date Searcher Picked Up: _____	____ Bibliographic	____ In-house sequence systems
Date Completed: _____	____ Litigation	____ Commercial _____ Oligomer _____ Score/Length
Searcher Prep & Review Time: _____	____ Fulltext	____ Interference _____ SPDI _____ Encode/Transl
Online Time: _____	____ Other	____ Other (specify)

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## UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS  
UNITED STATES PATENT AND TRADEMARK OFFICE  
WASHINGTON, D.C. 20231  
www.uspto.gov

Bib Data Sheet

<b>SERIAL NUMBER</b> 09/699,867	<b>FILING DATE</b> 10/30/2000 <b>RULE</b> -	<b>CLASS</b> 435	<b>GROUP ART UNIT</b> 1635	<b>ATTORNEY DOCKET NO.</b> 77473-12
<b>APPLICANTS</b> Jean-Pierre Perreault, Fleurimont, CANADA; Sirinart Ananvoranich, Westbury, CANADA; Daniel Lafontaine, Saint-Alexis de Montcalm, CANADA.				
<b>** CONTINUING DATA *****</b> THIS APPLICATION IS A CON OF PCT/CA99/00391 04/29/1999				
<b>** FOREIGN APPLICATIONS *****</b> CANADA 2230203 04/29/1998				
<b>IF REQUIRED, FOREIGN FILING LICENSE</b> <b>GRANTED ** 01/19/2001</b>				
<b>** SMALL ENTITY **</b>				
Foreign Priority claimed <input checked="" type="checkbox"/> yes <input type="checkbox"/> no 35 USC 119 (a-d) conditions met <input checked="" type="checkbox"/> yes <input type="checkbox"/> no <input type="checkbox"/> Met after Allowance	STATE OR COUNTRY CANADA	SHEETS DRAWING 7	TOTAL CLAIMS 19	INDEPENDENT CLAIMS 1
<b>ADDRESS</b> 22249				
<b>TITLE</b> Nucleic acid enzyme for RNA cleavage				
<b>FILING FEE RECEIVED</b> 420	FEES: Authority has been given in Paper No. _____ to charge/credit DEPOSIT ACCOUNT No. _____ for following:			
				<input type="checkbox"/> All Fees
				<input type="checkbox"/> 1.16 Fees ( Filing )
				<input type="checkbox"/> 1.17 Fees ( Processing Ext. of time )
				<input type="checkbox"/> 1.18 Fees ( Issue )
				<input type="checkbox"/> Other _____
				<input type="checkbox"/> Credit

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CRFE

10/26 0610 40

169207

10/27 45

10/28 20

# SEARCH REQUEST FORM

Thanks,

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 29, 2005, 08:49:56 ; Search time 792 Seconds  
(without alignments)  
594.397 Million cell updates/sec

Title: US-09-699-667E-61

Perfect score: 57  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9784742 seqs, 4129495052 residues

Total number of hits satisfying chosen parameters: 11492560

Minimum DB seq length: 0  
Maximum DB seq length: 150

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*

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28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24.4	42.8	52	18	US-10-346-880-40
2	24.4	42.8	52	18	US-10-346-880-80
3	24.4	42.8	52	18	US-10-150-407-40
4	24.4	42.8	52	18	US-10-150-407-80
5	24.4	42.8	50	9	US-09-733-042-12
					Sequence 40, Appl
					Sequence 80, Appl
					Sequence 40, Appl
					Sequence 80, Appl
					Sequence 12, Appl

#### ALIGNMENTS

RESULT 1  
US-10-346-880-40  
; Sequence 40, Application US/10346880  
; Publication No. US20030232035A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr., Thomas W  
; APPLICANT: Polo, John M  
; APPLICANT: Ibanez, Carlos E  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J  
; APPLICANT: Driver, David A  
; APPLICANT: Belli, Barbara A  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; FILE REFERENCE: EP01146.213 (CHIR-1146/11US)  
; CURRENT APPLICATION NUMBER: US/10/346,880  
; CURRENT FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: 09/503,138  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: 09/191,747  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 08/739,199  
; PRIOR FILING DATE: 1996-10-30  
; PRIOR APPLICATION NUMBER: 08/404,796  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: 08/376,184  
; PRIOR FILING DATE: 1995-01-18  
; PRIOR APPLICATION NUMBER: 08/348,472  
; PRIOR FILING DATE: 1994-11-30

c	6	24.4	42.8	90	9	US-09-733-042-13	Sequence 13, Appl
	7	24.4	42.8	90	10	US-09-190-246-2	Sequence 2, Appl
	8	24.4	42.8	91	16	US-10-237-302-7	Sequence 7, Appl
c	9	24.4	42.8	99	16	US-10-237-302-8	Sequence 8, Appl
	10	23	40.4	56	10	US-09-507-362-39	Sequence 39, Appl
	11	23	40.4	56	18	US-10-391-441-39	Sequence 39, Appl
	12	21	36.8	110	22	US-10-855-973-25	Sequence 25, Appl
c	13	20.6	36.1	130	21	US-10-425-115-163015	Sequence 163015,
	14	20	35.1	45	22	US-10-430-562-5	Sequence 5, Appl
	15	20	35.1	49	9	US-09-812-186-5	Sequence 5, Appl
	16	20	35.1	49	10	US-09-961-077-1234	Sequence 1234, Ap
	17	20	35.1	49	14	US-10-103-480-9	Sequence 9, Appl
	18	20	35.1	49	16	US-10-156-433-38	Sequence 38, Appl
	19	20	35.1	49	17	US-10-112-813-38	Sequence 38, Appl
c	20	19.8	34.7	60	10	US-09-908-975-6071	Sequence 6071, Ap
	21	19.6	34.4	60	10	US-09-908-975-13039	Sequence 13039, A
c	22	19.4	34.0	111	22	US-10-728-131-98	Sequence 98, Appl
	23	19	33.3	134	9	US-09-783-590-7012	Sequence 7012, Ap
c	24	18.4	32.3	119	10	US-09-835-9768-32	Sequence 32, Appl
	25	18.4	32.3	135	20	US-10-437-963-2147	Sequence 2147, Ap
c	26	18.2	31.9	103	9	US-09-837-992-10	Sequence 10, Appl
	27	18.2	31.9	103	26	US-11-128-026-10	Sequence 10, Appl
c	28	18.2	31.9	122	9	US-09-864-761-21127	Sequence 21127, A
	29	18.2	31.9	144	21	US-10-425-115-102935	Sequence 102935,
	30	18	31.6	47	19	US-10-380-438-10	Sequence 10, Appl
c	31	18	31.6	60	10	US-09-908-975-10629	Sequence 10629, A
	32	18	31.6	60	10	US-09-908-975-20125	Sequence 20125, A
	33	18	31.6	109	19	US-10-632-398-5	Sequence 5, Appl
c	34	18	31.6	112	18	US-10-402-841-1	Sequence 1, Appl
c	35	18	31.6	129	24	US-10-779-543-7614	Sequence 7614, Ap
	36	18	31.6	144	20	US-10-767-701-16350	Sequence 16350, A
c	37	17.8	31.2	115	17	US-10-029-386-26097	Sequence 26097, A
	38	17.8	31.2	123	19	US-10-425-114-4898	Sequence 4898, Ap
c	39	17.8	31.2	138	10	US-09-814-353-5007	Sequence 5007, Ap
	40	17.8	31.2	138	10	US-09-814-353-11299	Sequence 11299, A
c	41	17.6	30.9	70	18	US-10-403-232-6	Sequence 6, Appl
	42	17.6	30.9	75	17	US-10-259-678-163	Sequence 163, App
c	43	17.6	30.9	127	21	US-10-357-930-3957	Sequence 3957, Ap
	44	17.6	30.9	142	15	US-10-010-920-10	Sequence 10, Appl
c	45	17.6	30.9	142	15	US-10-010-920-11	Sequence 11, Appl

;; PRIOR APPLICATION NUMBER: 08/198,450  
;; PRIOR FILING DATE: 1994-02-18  
;; PRIOR APPLICATION NUMBER: 08/122,791  
;; PRIOR FILING DATE: 1993-09-15  
;; NUMBER OF SEQ ID NOS: 128  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 40  
;; LENGTH: 52  
;; TYPE: DNA  
;; ORGANISM: Unknown  
;; FEATURE:  
;; OTHER INFORMATION: Artificial sequence: nested primer HDV17-68  
US-10-346-880-40

Query Match 42.8%; Score 24.4; DB 18; Length 52;  
Best Local Similarity 59.4%; Pred. No. 17;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGCGGNNNNNNNUGGCGAUGC 35  
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 2  
US-10-346-880-80  
;; Sequence 80, Application US/10346880  
;; Publication No. US20030232035A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dubensky Jr., Thomas W  
;; APPLICANT: Polo, John M  
;; APPLICANT: Ibanez, Carlos E  
;; APPLICANT: Chang, Stephen M.W.  
;; APPLICANT: Jolly, Douglas J  
;; APPLICANT: Driver, David A  
;; APPLICANT: Belli, Barbara A  
;; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
;; FILE REFERENCE: PP01146.213 (CHIR-1146/11US)  
;; CURRENT APPLICATION NUMBER: US/10/346,880  
;; CURRENT FILING DATE: 2003-01-15  
;; PRIOR APPLICATION NUMBER: 09/503,138  
;; PRIOR FILING DATE: 2000-02-11  
;; PRIOR APPLICATION NUMBER: 09/191,747  
;; PRIOR FILING DATE: 1998-11-12  
;; PRIOR APPLICATION NUMBER: 08/739,199  
;; PRIOR FILING DATE: 1996-10-30  
;; PRIOR APPLICATION NUMBER: 08/404,796  
;; PRIOR FILING DATE: 1995-03-15  
;; PRIOR APPLICATION NUMBER: 08/376,184  
;; PRIOR FILING DATE: 1995-01-18  
;; PRIOR APPLICATION NUMBER: 08/348,472  
;; PRIOR FILING DATE: 1994-11-30  
;; PRIOR APPLICATION NUMBER: 08/198,450  
;; PRIOR FILING DATE: 1994-02-18  
;; PRIOR APPLICATION NUMBER: 08/122,791  
;; PRIOR FILING DATE: 1993-09-15  
;; NUMBER OF SEQ ID NOS: 128  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 80  
;; LENGTH: 52  
;; TYPE: DNA  
;; ORGANISM: Unknown  
;; FEATURE:  
;; OTHER INFORMATION: Artificial sequence: reverse primer HKV17-68  
US-10-346-880-80

Query Match 42.8%; Score 24.4; DB 18; Length 52;  
Best Local Similarity 59.4%; Pred. No. 17;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGCGGNNNNNNNUGGCGAUGC 35  
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32

RESULT 3  
US-10-150-407-40  
;; Sequence 40, Application US/10150407  
;; Publication No. US20040029278A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dubensky Jr, Thomas W  
;; Polo, John M.  
;; Jolly, Douglas J.  
;; Driver, David A.  
;; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
;; NUMBER OF SEQUENCES: 128  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SEED and BERRY LLP  
;; STREET: 6300 Columbia Center, 701 Fifth Avenue  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: US  
;; ZIP: 98104-7092  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/150,407  
;; FILING DATE: 17-May-2002  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/350,522  
;; FILING DATE: 08-Jul-1999  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McMasters, David D.  
;; REGISTRATION NUMBER: 33,963  
;; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031  
;; INFORMATION FOR SEQ ID NO: 40:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 52 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-10-150-407-40  
Query Match 42.8%; Score 24.4; DB 18; Length 52;  
Best Local Similarity 59.4%; Pred. No. 17;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
Qy 4 UCCACCUCCGCGGCGGNNNNNNNUGGCGAUGC 35  
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCCG 32  
RESULT 4  
US-10-150-407-80  
;; Sequence 80, Application US/10150407  
;; Publication No. US20040029278A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dubensky Jr, Thomas W  
;; Polo, John M.  
;; Jolly, Douglas J.  
;; Driver, David A.  
;; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
;; NUMBER OF SEQUENCES: 128  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SEED and BERRY LLP  
;; STREET: 6300 Columbia Center, 701 Fifth Avenue  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: US



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; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/150,407
; FILING DATE: 17-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,522
; FILING DATE: 08-Jul-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-150-407-80

Query Match 42.8%; Score 24.4; DB 18; Length 52;
Best Local Similarity 59.4%; Pred. No. 17;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCAUGCG 35
Db 1 TCCACCTCTCGCGGTCGACCTGGGCATCCG 32

RESULT 5
US-09-733-042-12
; Sequence 12, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 90
; TYPE: DNA
; ORGANISM: HDV-FOR
US-09-733-042-12

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Best Local Similarity 59.4%; Pred. No. 16;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCAUGCG 35
Db 22 TCCACCTCTCGCGGTCGACCTGGGCATCCG 53

RESULT 6
US-09-733-042-13/C
; Sequence 13, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
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; APPLICANT: Hennecke, Frank
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 90
; TYPE: DNA
; ORGANISM: HDV-REV
US-09-733-042-13

Query Match 42.8%; Score 24.4; DB 9; Length 90;
Best Local Similarity 59.4%; Pred. No. 16;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCAUGCG 35
Db 73 TCCACCTCTCGCGGTCGACCTGGGCATCCG 42

RESULT 7
US-09-190-246-2
; Sequence 2, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-2

Query Match 42.8%; Score 24.4; DB 10; Length 90;
Best Local Similarity 59.4%; Pred. No. 16;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCAUGCG 35
Db 22 TCCACCTCTCGCGGTCGACCTGGGCATCCG 53

RESULT 8
US-10-237-302-7
; Sequence 7, Application US/10237302
; Publication No. US20030119182A1
; GENERAL INFORMATION:
; APPLICANT: Alphavax, Inc.
; APPLICANT: Jonathan F. Smith
; APPLICANT: Kurt I. Kamrud
; APPLICANT: Jonathan O. Rayner
; APPLICANT: Sergey A. Dryga
; APPLICANT: Ian J. Caley
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
; FILE REFERENCE: 01113.0000202
; CURRENT APPLICATION NUMBER: US/10/237,302
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,722
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 7  
; LENGTH: 91  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =  
; OTHER INFORMATION: Synthetic Construct  
US-10-237-302-7

Query Match 42.8%; Score 24.4; DB 16; Length 91;  
Best Local Similarity 59.4%; Pred. No. 16;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGUNNNNNNUGGCAUGCG 35  
Db 18 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 49

RESULT 9  
US-10-237-302-8/c  
; Sequence 8, Application US/10237302  
; Publication No. US20030119182A1  
; GENERAL INFORMATION:  
; APPLICANT: AlphaVax, Inc.  
; APPLICANT: Jonathan F. Smith  
; APPLICANT: Kurt I. Kamrud  
; APPLICANT: Jonathan O. Rayner  
; APPLICANT: Sergey A. Dryga  
; APPLICANT: Ian J. Caley  
; TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS  
; FILE REFERENCE: 0113.0002U2  
; CURRENT APPLICATION NUMBER: US/10/237,302  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: 60/317,722  
; PRIOR FILING DATE: 2001-09-06  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 99  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =  
; OTHER INFORMATION: Synthetic Construct  
US-10-237-302-8

Query Match 42.8%; Score 24.4; DB 16; Length 99;  
Best Local Similarity 59.4%; Pred. No. 16;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGUNNNNNNUGGCAUGCG 35  
Db 78 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 47

RESULT 10  
US-09-507-362-39  
; Sequence 39, Application US/09507362  
; Publication No. US20030096397A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr., Thomas W.  
; Polo, John M.  
; Belli, Barbara A.  
; Schlesinger, Sondra  
; Dryga, Sergey A.  
; Frolov, Ilya  
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS  
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR  
; SYNTHESIS  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed Intellectual Property Law Group PLLC  
; STREET: 701 Fifth Avenue, Suite 6300

; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/507,362  
; FILING DATE: 18-Feb-2000  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 56 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-507-362-39

Query Match 40.4%; Score 23; DB 10; Length 56;  
Best Local Similarity 58.6%; Pred. No. 57;  
Matches 17; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGUNNNNNNUGGCAU 32  
Db 27 TCCACCTCTCGCGGTCCGACCTGGGCAT 55

RESULT 11  
US-10-391-441-39  
; Sequence 39, Application US/10391441  
; Publication No. US2003032058A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr., Thomas W.  
; Polo, John M.  
; Belli, Barbara A.  
; Schlesinger, Sondra  
; Dryga, Sergey A.  
; Frolov, Ilya  
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS  
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR  
; SYNTHESIS  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed Intellectual Property Law Group PLLC  
; STREET: 701 Fifth Avenue, Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/391,441  
; FILING DATE: 17-Mar-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/507,362  
; FILING DATE: 18-Feb-2000  
; ATTORNEY/AGENT INFORMATION:

NAME: McMaesters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 56 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Query Match 40.4%; Score 23; DB 18; Length 56;  
Best Local Similarity 58.6%; Pred. No. 57;  
Matches 17; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 4 UCCACUCCUCCGCGGUNNNNNNUGGCAU 32  
Db 27 TCCACCTCCTCGCGTCCGACCTGGCAT 55

RESULT 12  
US-10-855-975-25  
; Sequence 25, Application US/10855975  
; Publication No. US20050037487A1  
; GENERAL INFORMATION:  
; APPLICANT: Kawaoka, Yoshihiro  
; APPLICANT: Hamm, Stefan  
; APPLICANT: Ebihara, Hideki  
; TITLE OF INVENTION: WARF - Wisconsin Alumni Research Foundation  
; TITLE OF INVENTION: Recombinant Influenza Vectors with A PolII Promoter and Ribozymes  
; TITLE OF INVENTION: Vaccines and Gene Therapy  
; FILE REFERENCE: 800.037U51  
; CURRENT APPLICATION NUMBER: US/10/855.975  
; PRIOR FILING DATE: 2004-05-27  
; PRIOR APPLICATION NUMBER: US 60/473,797  
; PRIOR FILING DATE: 2003-05-28  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 110  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A synthetic HDV ribozyme sequence  
US-10-855-975-25

Query Match 36.8%; Score 21; DB 22; Length 110;  
Best Local Similarity 77.8%; Pred. No. 3.2e+02;  
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 UCCACUCCUCCGCGGUNNNNNNUGGC 30  
Db 67 UCCACUCCUCCGCGGCGGACCGGCGGC 93

RESULT 13  
US-10-425-115-163015/c  
; Sequence 163015, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425.115  
; CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 163015  
; LENGTH: 130  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_80243C.1  
US-10-425-115-163015

Query Match 36.1%; Score 20.6; DB 21; Length 130;  
Best Local Similarity 49.1%; Pred. No. 4.5e+02;  
Matches 28; Conservative 4; Mismatches 25; Indels 0; Gaps 0;

Qy 1 GGGUCCACUCCUCCGCGGUNNNNNNUGGCAUGCGCUUCGCAUGGCUAAGGGGACCC 57  
Db 112 GGGCGCACCATGTCCGGTCTTTTGTAGCCAAGACTTCGGCACACGCCGTGGGACGC 56

RESULT 14  
US-10-430-562-5  
; Sequence 5, Application US/10430562  
; Publication No. US20050074760A1  
; GENERAL INFORMATION:  
; APPLICANT: Matulic-Adamic, Jasenka  
; Beigelman, Leonid  
; Karpeisky, Alexander  
; Jarvis, Thale  
; Usman, Nassim  
; Dizenzo, Anthony  
; Wincott, Francine  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACIDS CONTAINING  
5'-AND/OR 3'-CAP STRUCTURES

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/430.562  
FILING DATE: 06-May-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/632.882  
FILING DATE: April 16, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 217/226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: The letter "N" stands for  
any base  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-430-562-5





```
;
;
; 4 UCCACCUCGCGGNNNNNNUGGCAUGGCGUUCGCAUGGCUAAGGGACC 56
; |||||
; 8 UCCACCUCGCGGCGGCAUGGCGCAU----CUUCGGAUGGCUAAGGGAGC 56
; |||||

RESULT 2
US-08-741-881-40
; Sequence 40, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; City: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-40

Query Match 42.8%; Score 24.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.6;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

;
;
; 4 UCCACCUCGCGGNNNNNNUGGCAUGGCG 35
; :|||||:|||||:
; 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
; :|||||:|||||:

RESULT 3
US-08-741-881-80
; Sequence 80, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
```

```
;
;
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; City: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-80

Query Match 42.8%; Score 24.4; DB 1; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.6;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

;
;
; 4 UCCACCUCGCGGNNNNNNUGGCAUGCG 35
; :|||||:|||||:
; 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
; :|||||:|||||:

RESULT 4
US-08-739-158-40
; Sequence 40, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; City: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELECOMMUNICATION INFORMATION:
```

RESULT 6  
US-08-739-167-40  
; Sequence 40, Application US/08739167

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 30-OCT-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049,423C7 / 1146.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 52 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-739-167-80

Query Match 42.8%; Score 24.4; DB 2; Length 52;  
Best Local Similarity 59.4%; Pred. No. 4.6;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGGGUNNNNNUGGCGCAUGCG 35  
DB 1 TCCACCTCTCCGGGTCGACCTGGGCATCCG 32

RESULT 8  
US-08-404-796-40  
; Sequence 40, Application US/08404796  
; Patent No. 6015686  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 15-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049,423C5 / 1146.006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 52 base pairs  
; TYPE: nucleic acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-404-796-40  
Query Match 42.8%; Score 24.4; DB 3; Length 52;  
Best Local Similarity 59.4%; Pred. No. 4.6;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
QY 4 UCCACUCCUCCGGGUNNNNNUGGCGCAUGCG 35  
DB 1 TCCACCTCTCCGGGTCGACCTGGGCATCCG 32

RESULT 9  
US-08-404-796-80  
; Sequence 80, Application US/08404796  
; Patent No. 6015686  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/404,796  
; FILING DATE: 15-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049,423C5 / 1146.006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 52 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-404-796-80

Query Match 42.8%; Score 24.4; DB 3; Length 52;  
Best Local Similarity 59.4%; Pred. No. 4.6;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 4 UCCACUCCUCCGGGUNNNNNUGGCGCAUGCG 35  
DB 1 TCCACCTCTCCGGGTCGACCTGGGCATCCG 32

RESULT 10  
US-08-931-869-40  
; Sequence 40, Application US/08931869  
; Patent No. 6015694  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W



APPLICANT: Polo, John M.  
APPLICANT: Ibanez, Carlos E.  
APPLICANT: Chang, Stephen M.W.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
APPLICANT: Belli, Barbara A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,869  
FILING DATE: 16-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/404,796  
FILING DATE: 15-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-931-869-40  
Query Match 42.8%; Score 24.4; DB 3; Length 52;  
Best Local Similarity 59.4%; Pred. No. 4.6;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGCG 35  
Db 1 TCCACCTCTCGCGGTCGCGACCTGGCGATCCG 32  
RESULT 11  
US-08-931-869-80  
Sequence 80, Application US/08931869  
Patent No. 6015694  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Ibanez, Carlos E.  
APPLICANT: Chang, Stephen M.W.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
APPLICANT: Belli, Barbara A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,399  
FILING DATE: 08-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52 base pairs  
TYPE: nucleic acid  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,869  
FILING DATE: 16-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/404,796  
FILING DATE: 15-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-931-869-80  
Query Match 42.8%; Score 24.4; DB 3; Length 52;  
Best Local Similarity 59.4%; Pred. No. 4.6;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
QY 4 UCCACUCCUCCGCGGNNNNNUGGCGAUGCG 35  
Db 1 TCCACCTCTCGCGGTCGCGACCTGGCGATCCG 32  
RESULT 12  
US-09-350-399-40  
Sequence 40, Application US/09350399  
Patent No. 6342372  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,399  
FILING DATE: 08-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52 base pairs  
TYPE: nucleic acid

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/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-350-399-40

Query Match 42.8%; Score 24.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.6;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGUNNNNNNUGGCAUGCG 35
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 13
US-09-350-399-80
; Sequence 80, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Jolly, Douglas J.
; Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMaisters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-350-399-80

Query Match 42.8%; Score 24.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.6;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGUNNNNNNUGGCAUGCG 35
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 14
US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
```

```
/
/ Ibanez, Carlos E.
/ Chang, Stephen M.W.
/ Jolly, Douglas J.
/ Driver, David A.
/ Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
; STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
; CITY: NEWPORT BEACH
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,140A
; FILING DATE: 22-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cullman, Louis C.
; REGISTRATION NUMBER: 39,645
; REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (949) 823.6000
; TELEFAX: (949) 823.6100
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-236-140A-40

Query Match 42.8%; Score 24.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.6;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGUNNNNNNUGGCAUGCG 35
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 15
US-09-236-140A-80
; Sequence 80, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
; Ibanez, Carlos E.
; Chang, Stephen M.W.
; Jolly, Douglas J.
; Driver, David A.
; Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
; STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
; CITY: NEWPORT BEACH
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,140A
; FILING DATE: 22-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cullman, Louis C.
; REGISTRATION NUMBER: 39,645
; REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (949) 823.6000
; TELEFAX: (949) 823.6100
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-236-140A-80

Query Match          42.8%; Score 24.4; DB 3; Length 52;
Best Local Similarity 59.4%; Pred. No. 4.6;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy      4 UCCACCUCCUGCGGUNNNNNNUGGCGAUGCG 35
      :|||||:|||||:|||||:
Db      1 TCCACCTCCTCGCGTCCGACCTGGGCATCG 32
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
748.171 Million cell updates/sec

Title: US-09-699-667E-61  
Perfect score: 57  
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Scoring table: IDENTITY NUC  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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4: Geneseqn2001as:\*  
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6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
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11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	51	89.5	57	AAZ57636	Aaz57636 Trans-act
2	51	89.5	57	AAZ57637	Aaz57637 Trans-act
3	41.4	72.6	57	AAZ57638	Aaz57638 Trans-act
4	29.4	51.6	37	AAZ57639	Aaz57639 Nucleotid
5	25.8	45.3	61	AAQ46667	Aaq46667 Substrate
6	24.4	42.8	48	ADRA7040	Adr7040 Dengue vi
7	24.4	42.8	48	ADTA8985	Adt48985 PCR prime
8	24.4	42.8	51	AAQ86173	Aaq86173 Primer HD
9	24.4	42.8	52	AAQ86204	Aaq86204 Sindbis/H
10	24.4	42.8	52	AAT31151	Aat31151 HDV rever
11	24.4	42.8	52	AAT30817	Aat30817 HDV riboz
12	24.4	42.8	52	AAV42394	Aav42394 Nested PC
13	24.4	42.8	52	AAV42426	Aav42426 Forward P
14	24.4	42.8	52	AAV60154	Aav60154 Nested PC
15	24.4	42.8	52	AAV60185	Aav60185 Reverse P
16	24.4	42.8	52	AAV70746	Aav70746 Reverse P
17	24.4	42.8	52	AAV70714	Aav70714 Nested pr
18	24.4	42.8	52	AAZ92930	Aaz92930 Hepatitis
19	24.4	42.8	52	AAZ92970	Aaz92970 Hepatitis
20	24.4	42.8	52	AAZ92843	Aaz92843 Hepatitis

21	24.4	42.8	52	3	AAZ92803	Aaz92803 Hepatitis
22	24.4	42.8	52	6	AAU38850	Aal38850 Alphaviru
23	24.4	42.8	52	6	AAU38810	Aal38810 Alphaviru
24	24.4	42.8	52	6	ABK46276	Abk46276 HDV anti
25	24.4	42.8	52	6	ABK46316	Abk46316 Hepatitis
26	24.4	42.8	52	12	ADI30383	Adi30383 Hepatitis
27	24.4	42.8	52	12	ADI30423	Adi30423 Hepatitis
28	24.4	42.8	52	12	ADO13982	Ado13982 Eukaryoti
29	24.4	42.8	52	12	ADO13942	Ado13942 Eukaryoti
30	24.4	42.8	57	12	ADH10551	Adh10551 Hepatitis
31	24.4	42.8	80	2	AAQ53138	Aaq53138 Substrate
32	24.4	42.8	80	2	AAQ53140	Aaq53140 Substrate
33	24.4	42.8	83	5	AAZ28121	Aaf28121 HDV riboz
34	24.4	42.8	84	13	ADR47033	Adr7033 Dengue vi
35	24.4	42.8	85	2	AAQ46665	Aaq46665 Self-clea
36	24.4	42.8	86	2	AAQ46663	Aaq46663 Self-clea
37	24.4	42.8	90	2	AAQ76586	Aax76586 Hepatitis
38	24.4	42.8	90	5	AAQ84035	Aaf84035 EPO gene
39	24.4	42.8	90	5	AAQ84036	Aaf84036 EPO gene
40	24.4	42.8	91	8	ABZ82120	Abz82120 Hepatitis
41	24.4	42.8	94	12	ADP96249	Adp96249 HEP rabie
42	24.4	42.8	99	8	ABZ82121	Abz82121 Hepatitis
43	23	40.4	56	2	AAQ59264	Aax59264 Nested pr
44	23	40.4	56	2	AAQ58506	Aax58506 Nested pr
45	23	40.4	56	8	ABX81463	Abx81463 Sindbis v

ALIGNMENTS

RESULT 1  
AAZ57636  
ID AAZ57636 standard; RNA; 57 BP.  
XX  
AC AAZ57636;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Trans-acting antigenomic delta ribozyme, deltaRzPl.1 nucleotide sequence.  
XX  
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;  
KW inherited disease; deltaRzPl.1; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_binding 1..6  
FT /tag= a  
FT /note= "Forms double stranded region with bases 52-57"  
FT stem\_loop 7..19  
FT /tag= b  
FT misc\_binding 20..25  
FT /tag= c  
FT /bound moiety= "SP1.1 substrate (AAZ57641) bases 5-11"  
FT stem\_loop 30..45  
FT /tag= d  
FT misc\_binding 52..57  
FT /tag= e  
FT /note= "Forms a double stranded region with bases 6-1"  
XX  
WO9955856-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 29-APR-1999; 99WO-CA000391.  
XX  
PR 29-APR-1998; 98CA-02230203.  
XX  
PA (UYSH ) UNIV SHERBROOKE.  
XX  
PI Perreault J, Ananvoranich S, Lafontaine D;  
DR WPI; 2000-096791/08.

```
XX
PT New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.
XX
PS Example 1; Fig 1A; 52pp; English.
XX
CC This is the nucleotide sequence of ribozyme deltaRzPl.1. This ribozyme
CC cleaves substrate Sp1.1 (see AA257641). The invention relates to a
CC nucleic acid enzyme (e.g. deltaRzPl.1) that is constructed to have a
CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
CC substrate of the enzyme has the sequence 5'-H*GNHNN-3'. The binding
CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC cleavage site of the substrate (cleavage site is represented by *). At
CC least one nucleotide is present 5' to the cleavage site of the substrate
CC sequence. The enzyme of the invention is used to cleave a substrate
CC nucleotide sequence at a specific cleavage site by mixing the substrate
CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications
XX
SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
Query Match 89.5%; Score 51; DB 3; Length 57;
Best Local Similarity 89.5%; Pred. No. 9e-09;
Matches 51; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GGGUCCACCUCCGCGGUNNNNUGGCAUGCGGCUUGGCUAAGGGACCC 57
Db 1 GGGUCCACCUCCGCGGCUUGGCAUGCGGCUUGGCUAAGGGACCC 57
RESULT 2
AAZ57637
ID AAZ57637 standard; RNA; 57 BP.
AC AAZ57637;
XX
DT 05-APR-2000 (first entry)
XX
DE Trans-acting antigenomic delta ribozyme, deltaRzPl.2 nucleotide sequence.
XX
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; deltaRzPl.2; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 1..6
FT /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /tag= b
FT misc_binding 20..25
FT /tag= c
FT stem_loop 30..45
FT /tag= d
FT misc_binding 52..57
FT /tag= e
FT /note= "Forms a double stranded region with bases 6-1"
XX
FN WO9955856-A2.
XX
PD 04-NOV-1999.
XX
PF 29-APR-1999; 99WO-CA000391.
XX
PR 29-APR-1998; 98CA-02230203.
XX
PA (UYSH ) UNIV SHERBROOKE.
XX
PI Perreault J, Ananvoranich S, Lafontaine D;
XX
```

```
DR WPI; 2000-096791/08.
XX
PT New construction of nucleic acid enzyme useful for biotechnological,
PT diagnostic and therapeutic applications.
XX
PS Example 1; Page; 52pp; English.
XX
CC This is the nucleotide sequence of ribozyme deltaRzPl.2. This ribozyme
CC cleaves substrate Sp1.2 (see AA257634). The invention relates to a
CC nucleic acid enzyme (e.g. deltaRzPl.2) that is constructed to have a
CC substrate binding portion with the following sequence 3'-UNNXXN-5'. The
CC substrate of the enzyme has the sequence 5'-H*GNHNN-3'. The binding
CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the
CC cleavage site of the substrate (cleavage site is represented by *). At
CC least one nucleotide is present 5' to the cleavage site of the substrate
CC sequence. The enzyme of the invention is used to cleave a substrate
CC nucleotide sequence at a specific cleavage site by mixing the substrate
CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing
CC for example an inherited disease. The enzymes also have other
CC therapeutic, biotechnological and diagnostic applications. Note: This
CC sequence is not shown in the specification, but has been derived from the
CC deltaRzPl.1 sequence (AA257636) shown in figure 1
XX
SQ Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
Query Match 89.5%; Score 51; DB 3; Length 57;
Best Local Similarity 89.5%; Pred. No. 9e-09;
Matches 51; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GGGUCCACCUCCGCGGUNNNNUGGCAUGCGGCUUGGCUAAGGGACCC 57
Db 1 GGGUCCACCUCCGCGGCUUGGCAUGCGGCUUGGCUAAGGGACCC 57
RESULT 3
AAZ57638
ID AAZ57638 standard; RNA; 57 BP.
AC AAZ57638;
XX
DT 15-SEP-2003 (revised)
DT 05-APR-2000 (first entry)
XX
DE Trans-acting antigenomic delta ribozyme nucleotide sequence.
XX
KW Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
KW inherited disease; ss.
XX
OS Hepatitis D virus.
XX
FH Key Location/Qualifiers
FT misc_binding 1..6
FT /tag= a
FT /note= "Forms double stranded region with bases 52-57"
FT stem_loop 7..19
FT /tag= b
FT misc_binding 20..25
FT /tag= c
FT stem_loop 30..45
FT /tag= d
FT misc_binding 52..57
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XX
FN WO9955856-A2.
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PD 04-NOV-1999.
XX
PF 29-APR-1999; 99WO-CA000391.
XX
PR 29-APR-1998; 98CA-02230203.
XX
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PA (UYSH ) UNIV SHERBROOKE.  
 XX Perreault J, Ananvoranich S, Lafontaine D;  
 PI WPI; 2000-096791/08.  
 XX New construction of nucleic acid enzyme useful for biotechnological,  
 PT diagnostic and therapeutic applications.  
 XX Example 1; Fig 2; 52pp; English.  
 XX This is the nucleotide sequence of a trans-acting antigenomic delta  
 CC ribozyme of the invention. This ribozyme cleaves substrate SPI.1 (see  
 CC AAZ57641). The invention relates to a nucleic acid enzyme (e.g.  
 CC deltaRZP1.1) that is constructed to have a substrate binding portion with  
 CC the following sequence 3'-UNNXNN-5'. The substrate of the enzyme has the  
 CC sequence 5'-H'\*GNNHN-3'. The binding portion of the enzyme (ribozyme)  
 CC base pairs to 6 nucleotides 3' to the cleavage site of the substrate  
 CC (cleavage site is represented by \*). At least one nucleotide is present  
 CC 5' to the cleavage site of the substrate sequence. The enzyme of the  
 CC invention is used to cleave a substrate nucleotide sequence at a specific  
 CC cleavage site by mixing the substrate with the enzyme. The enzyme is used  
 CC to cleave viral RNA or RNA causing for example an inherited disease. The  
 CC enzymes also have other therapeutic, biotechnological and diagnostic  
 CC applications. (Updated on 15-SEP-2003 to standardise OS field)  
 XX  
 XX Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;  
 SQ  
 Query Match 72.6%; Score 41.4; DB 3; Length 57;  
 Best Local Similarity 78.9%; Pred. No. 2.6e-05;  
 Matches 45; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 OY 1 GGGUCCACCUCUCCGGGUNNNNNNUGGCAUGCGGCUUGGCUAAGGACCC 57  
 DB 1 GGGUCCACCUCUCCGGGUNNNNNNUGGCAUGCGGCUUGGCUAAGGACCC 57  
 RESULT 4  
 AAZ57639  
 ID AAZ57639 standard; RNA; 37 BP.  
 AC AAZ57639;  
 XX  
 XX 05-APR-2000 (first entry)  
 DT Nucleotide sequence of bimolecular ribozyme RZA fragment.  
 DE Bimolecular ribozyme; viral RNA cleavage; RZA fragment;  
 XX Inherited disease; ss.  
 KW Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_binding 1..6  
 FT /<tag= a  
 FT /bound moiety= "RzB fragment of bimolecular ribozyme"  
 FT /note= "Forms double-stranded region with bases 20-16 of  
 FT sequence AAZ57640"  
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 FT stem\_loop 7..19  
 FT /<tag= b  
 FT /bound moiety= "RzB fragment of bimolecular ribozyme"  
 FT /note= "Forms double-stranded region with bases 11-6 of  
 FT sequence AAZ57641"  
 FT  
 FT misc\_binding 30..37  
 FT /<tag= d  
 FT /bound moiety= "RzB fragment of bimolecular ribozyme"  
 FT /note= "Forms double-stranded region with bases 8-1 of  
 FT sequence AAZ57640"  
 FT  
 XX W09955856-A2.  
 XX

PD 04-NOV-1999.  
 XX 29-APR-1999; 99WO-CA000391.  
 XX 29-APR-1998; 98CA-02230203.  
 XX (UYSH ) UNIV SHERBROOKE.  
 XX Perreault J, Ananvoranich S, Lafontaine D;  
 XX WPI; 2000-096791/08.  
 XX New construction of nucleic acid enzyme useful for biotechnological,  
 PT diagnostic and therapeutic applications.  
 XX Example 5; Fig 4; 52pp; English.  
 XX This is the nucleotide sequence bimolecular ribozyme RZA fragment. This  
 CC ribozyme cleaves substrate SPI.1 (see AAZ57641). The invention relates to  
 CC a nucleic acid enzyme (e.g. deltaRZP1.1) that is constructed to have a  
 CC substrate binding portion with the following sequence 3'-UNNXNN-5'. The  
 CC substrate of the enzyme has the sequence 5'-H'\*GNNHN-3'. The binding  
 CC portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the  
 CC cleavage site of the substrate (cleavage site is represented by \*). At  
 CC least one nucleotide is present 5' to the cleavage site of the substrate  
 CC sequence. The enzyme of the invention is used to cleave a substrate  
 CC nucleotide sequence at a specific cleavage site by mixing the substrate  
 CC with the enzyme. The enzyme is used to cleave viral RNA or RNA causing  
 CC for example an inherited disease. The enzymes also have other  
 CC therapeutic, biotechnological and diagnostic applications  
 XX  
 XX Sequence 37 BP; 3 A; 16 C; 12 G; 0 T; 6 U; 0 Other;  
 SQ  
 Query Match 51.6%; Score 29.4; DB 3; Length 37;  
 Best Local Similarity 81.1%; Pred. No. 0.5;  
 Matches 30; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 OY 1 GGGUCCACCUCUCCGGGUNNNNNNUGGCAUGCGGCGC 37  
 DB 1 GGGUCCACCUCUCCGGGUNNNNNNUGGCAUGCGGCGC 37  
 RESULT 5  
 AAQ46667  
 ID AAQ46667 standard; RNA; 61 BP.  
 AC AAQ46667;  
 XX 25-MAR-2003 (revised)  
 DT 13-JAN-1994 (first entry)  
 DE Substrate-cleaving sequence ADC3.  
 XX Substrate; self-cleaving sequence; HDV; hepatitis delta virus; enzyme;  
 KW duplex; ss.  
 XX Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT stem\_loop 7..55  
 FT /<tag= a  
 FT misc\_structure 7..10  
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 FT /label= stem II  
 FT /note= "forms duplex with region 52..55"  
 FT stem\_loop 11..23  
 FT /<tag= d  
 FT misc\_structure 11..13  
 FT /<tag= e  
 FT /label= stem III  
 FT /note= "forms duplex with region 21..23"  
 FT misc\_feature 21..23  
 FT /<tag= f

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FT FT /label= stem_III
FT FT /note= "forms duplex with region 11. .13"
FT FT 24. .30
FT FT /tag= g
FT FT /note= "RNA substrate binding region"
FT FT 33. .37
FT FT /tag= i
FT FT /label= stem_IV
FT FT /note= "forms duplex with region 42. .45"
FT FT 34. .45
FT FT /tag= h
FT FT /tag= j
FT FT /label= stem_IV
FT FT /note= "forms duplex with region 33. .37"
FT FT 52. .55
FT FT /tag= c
FT FT /label= stem_II
FT FT /note= "forms duplex with region 7. .10"
FT FT
XX XX WO9314218-A1.
XX XX 22-JUL-1993.
XX XX 12-JAN-1993; 93WO-US000292.
XX XX 13-JAN-1992; 92US-00821155.
XX XX (UYDU-) UNIV DUKE.
XX XX Been MD, Rosenstein SP, Perrota AT;
XX XX WPI; 1993-243233/30.
XX XX
XX XX Nucleic acid molecule having RNA substrate-cleaving enzymatic activity -
XX XX useful for cleaving specific target molecules in-vitro.
XX XX Disclosure; Fig 8; 55pp; English.
XX XX
XX XX The self-cleaving sequences from genomic and antigenomic HDV can be used
XX XX to develop enzymatic RNA mols. with similar properties. ADC3 is a smaller
XX XX version of ADC1 (AAQ53138), wherein stem IV is shortened. Such a smaller
XX XX enzymatic RNA has simplified synthesis and the potential for higher
XX XX specific activity due to a higher probability that a small RNA will fold
XX XX into an enzymatically active structure. (Updated on 25-MAR-2003 to
XX XX correct PN field.)
XX XX
XX XX Sequence 61 BP; 10 A; 20 C; 19 G; 0 T; 12 U; 0 Other;
XX XX
XX XX Query Match 45.3%; Score 25.8; DB 2; Length 61;
XX XX Best Local Similarity 77.4%; Pred. No. 11;
XX XX Matches 41; Conservative 0; Mismatches 8; Indels 4; Gaps 1;
XX XX
Qy 4 UCCACCUCUCGCGGNNNNNUGGCAUGCGGCUUGCGCAUGGCUAAGGGACC 56
Db 8 UCCACCUCUCGCGGCUUGCGGCAU-----CUUCGGAUGGCUAAGGGAGC 56
XX XX
RESULT 6
AD47040
ID ADR47040 standard; DNA; 48 BP.
XX XX
AC ADR47040;
XX XX
DT 18-NOV-2004 (first entry)
XX XX
DE Dengue virus vaccine oligonucleotide #15.
XX XX
KW ss: cytotostatic; virucide; dengue virus; recombinant replicon; deletion;
KW prem protein; C protein; NS1 protein signal; vaccine; cervical cancer;
KW viral disease; antigen; dendritic cell; immune response;
KW human papillomavirus.
XX XX

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OS Unidentified.
XX XX
PN WO2004072274-A1.
XX XX
PD 26-AUG-2004.
XX XX
XX 30-JAN-2004; 2004WO-CN000088.
XX XX
XX 30-JAN-2003; 2003CN-00115272.
XX XX
XX 30-JAN-2003; 2003CN-00115273.
XX XX
XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
XX XX (TENG-) TENGGEN BIOMEDICAL CO.
XX XX (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX XX
XX Pang X;
XX XX
XX WPI; 2004-625870/60.
XX XX
XX Virus-like particle vaccines containing dengue virus recombinant replicon
XX XX as core for carrier, applicable in preventives or/and remedies for tumors
XX XX like cervical cancer and viral diseases.
XX XX
XX Example 4; SEQ ID NO 37; 38pp; Chinese.
XX XX
XX A dengue virus recombinant replicon has a deletion of the complete coding
XX XX sequence for preM protein of dengue virus and also includes elements of
XX XX e.g. the non-coding region in the whole of the 5'-end, the coding region
XX XX of the front 20 amino acids in the C protein, and the coding region of
XX XX NS1 protein signal; coding regions of all non-structural proteins. The
XX XX obtained vaccines are useful in producing preventives or/and remedies for
XX XX cancer like cervical cancer and viral diseases. Such vaccines can
XX XX efficiently express antigen in infected cells, which is because dengue
XX XX virus can infect dendritic cells, and can effectively present antigen to
XX XX provide immunity effect. Different types of dengue virus can be used to
XX XX repeatedly produce efficient immune response thereby strengthening the
XX XX body's immune system against the pathogen that contains such antigen.
XX XX Human papillomavirus (HPV) vaccines were prepared by using a gene-
XX XX expressing system using of the full-length dengue virus cDNA clone
XX XX (P8S/PLD2). The recombinant virus vectors were transfected into baby
XX XX hamster kidney (BHK) cells to enable the screening of BHK-21 ret-off cell
XX XX lines. This sequence corresponds to an oligonucleotide used in the
XX XX recombinant replicon of the invention.
XX XX
XX XX Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;
XX XX
XX XX Query Match 42.8%; Score 24.4; DB 13; Length 48;
XX XX Best Local Similarity 59.4%; Pred. No. 33;
XX XX Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
XX XX
Qy 4 UCCACCUCUCGCGGNNNNNUGGCAUGCG 35
Db 17 TCCACCTCTCTCGGCTCCGACCTGGGCATCCG 48
XX XX
RESULT 7
ADT48965
ID ADT48965 standard; DNA; 48 BP.
XX XX
AC ADT48965;
XX XX
XX 16-DEC-2004 (first entry)
XX XX
XX PCR primer 5' HDVr, seq id 29.
XX XX
XX Virucide; Japanese encephalitis B virus; bivalent vaccine; hepatitis B;
XX XX PCR; primer; ss.
XX XX
XX Viruses.
XX XX
XX WO2004082712-A1.
XX XX
XX 30-SEP-2004.
XX XX

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XX PF 19-MAR-2004; 2004WO-CN000232.  
 XX PR 20-MAR-2003; 2003CN-00115912.  
 XX PA (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.  
 XX PA (TENG-) TENGGEN BIOMEDICAL CO.  
 XX PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.  
 XX PI Pang X;  
 XX DR WPI; 2004-699719/68.  
 XX DR  
 XX PT Bivalent vaccines for preventing and treating Japanese (B) encephalitis  
 PT and hepatitis B produced by recombinant technique using encephalitis B  
 PT virus as vector to express antigen gene of hepatitis B.  
 XX PS  
 XX PS Example 8; SEQ ID NO 29; 33pp; Chinese.  
 XX CC The invention relates to a recombinant Japanese encephalitis B virus  
 CC constructed from encephalitis B virus and a recombinant genome, where the  
 CC genome is inserted with an exogenous nucleotide sequence for  
 CC recombination and capable of retaining its self-replication function. The  
 CC virus is useful in producing the bivalent vaccines for preventing and  
 CC treating Japanese (B) encephalitis and hepatitis B. Such vaccines are  
 CC recombinant virus can efficiently express the antigen of hepatitis B  
 CC virus with the safety and immunogenicity of attenuated encephalitis B  
 CC virus vaccines. The current sequence represents a PCR primer used in an  
 CC example from the invention.  
 XX CC  
 XX SQ Sequence 48 BP; 5 A; 19 C; 15 G; 9 T; 0 U; 0 Other;  
 Query Match 42.8%; Score 24.4; DB 13; Length 48;  
 Best Local Similarity 59.4%; Pred. No. 33;  
 Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 QY 4 UCCACCUCUCCGCGGUNNNNNUGGCAUCG 35  
 :|||:||||:||||:||||:||  
 Db 17 TCCACCTCTCGGCGTCCGACCTGGCATCCG 48  
 RESULT 8  
 AAQ86173  
 ID AAQ86173 standard; DNA; 51 BP.  
 AC AAQ86173;  
 XX 25-MAR-2003 (revised)  
 DT 21-NOV-1995 (first entry)  
 XX  
 DE Primer HDV17-68 amplifies vector DNA to initiate Sindbis infection.  
 XX  
 KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;  
 KW transcription initiation; non-structural protein; subgenomic fragment;  
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;  
 KW primer; polymerase chain reaction; cystic fibrosis; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9507994-A2.  
 XX  
 XX 23-MAR-1995.  
 XX  
 XX 15-SEP-1994; 94WO-US010469.  
 XX  
 XX 15-SEP-1993; 93US-00122791.  
 PR 18-FEB-1994; 94US-00198450.  
 XX  
 XX (VIAG-) VIAGENE INC.  
 XX  
 XX Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;  
 XX WPI; 1995-131362/17.  
 XX  
 XX New alpha virus vectors for gene therapy - of viral infection, cancer,  
 XX auto-immune disease, etc., and as vaccines.  
 XX Example 7; Page 114; 260pp; English.  
 XX  
 XX The sequences given in AAQ86200-15 are primers which were used in the  
 XX production of alphavirus vectors expressing multiple heterologous genes.  
 XX These vectors are eukaryotic layered vector initiation systems (ELVIS)

DR WPI; 1995-131362/17.  
 XX  
 XX New alpha virus vectors for gene therapy - of viral infection, cancer,  
 PT auto-immune disease, etc., and as vaccines.  
 XX  
 XX Example 2; Page 68; 260pp; English.  
 PS  
 XX  
 XX The sequences given in AAQ86167-81 are primers which were used in the  
 CC generation of plasmid DNA which initiates Sindbis infection. The  
 CC amplified DNA sequences were used in the construction of a eukaryotic  
 CC layered vector initiation system (ELVIS) derived from Sindbis. ELVIS's  
 CC comprise a 5' sequence capable of initiating transcription of an  
 CC alphavirus, a nucleotide sequence encoding alphavirus non-structural  
 CC proteins, a viral junction region which has been inactivated such that  
 CC viral transcription of the subgenomic fragment is prevented, and an  
 CC alphavirus RNA polymerase recognition sequence. Inactivation of the viral  
 CC junction region prevents transcription of the subgenomic fragment making  
 CC vectors such as this suitable for a wide variety of applications, eg.  
 CC gene therapy for the treatment of cystic fibrosis. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX  
 XX SQ Sequence 51 BP; 9 A; 20 C; 14 G; 8 T; 0 U; 0 Other;  
 Query Match 42.8%; Score 24.4; DB 2; Length 51;  
 Best Local Similarity 59.4%; Pred. No. 33;  
 Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 QY 4 UCCACCUCUCCGCGGUNNNNNUGGCAUCG 35  
 :|||:||||:||||:||||:||  
 Db 1 TCCACCTCTCGGCGTCCGACCTGGCATCCG 32  
 RESULT 9  
 AAQ86204  
 ID AAQ86204 standard; DNA; 52 BP.  
 XX  
 XX AAQ86204;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 23-NOV-1995 (first entry)  
 XX  
 XX Sindbis/HDV ribozyme sequence reverse primer, HDV17-68.  
 DE  
 XX  
 KW Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;  
 KW transcription initiation; non-structural protein; subgenomic fragment;  
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;  
 KW primer; polymerase chain reaction; cystic fibrosis; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9507994-A2.  
 XX  
 XX 23-MAR-1995.  
 XX  
 XX 15-SEP-1994; 94WO-US010469.  
 XX  
 XX 15-SEP-1993; 93US-00122791.  
 PR 18-FEB-1994; 94US-00198450.  
 XX  
 XX (VIAG-) VIAGENE INC.  
 XX  
 XX Dubensky TW, Ibanez CE, Chang SM, Jolly DJ, Driver DA, Polo JM;  
 XX WPI; 1995-131362/17.  
 XX  
 XX New alpha virus vectors for gene therapy - of viral infection, cancer,  
 PT auto-immune disease, etc., and as vaccines.  
 XX  
 XX Example 7; Page 114; 260pp; English.  
 XX  
 XX The sequences given in AAQ86200-15 are primers which were used in the  
 XX production of alphavirus vectors expressing multiple heterologous genes.  
 XX These vectors are eukaryotic layered vector initiation systems (ELVIS)

CC derived from Sindbis. ELVIS's comprise a 5' sequence capable of  
 CC initiating transcription of an alphavirus, a nucleotide sequence encoding  
 CC alphavirus non-structural proteins, a viral junction region which has  
 CC been inactivated such that viral transcription of the subgenomic fragment  
 CC is prevented, and an alphavirus RNA polymerase recognition sequence.  
 CC inactivation of the viral junction region prevents transcription of the  
 CC subgenomic fragment making vectors such as this suitable for a wide  
 CC variety of applications, eg. gene therapy for the treatment of cystic  
 CC fibrosis. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 42.8%; Score 24.4; DB 2; Length 52;  
 Best Local Similarity 59.4%; Pred. No. 33;  
 Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCGCAUGCG 35  
 :||||:||||:||||:||||:||||:||||:||||:  
 Db 1 TCCACCTCTCGCGGTCGCGACCTGGCATCCG 32

RESULT 10  
 AAT31151  
 ID AAT31151 standard; DNA; 52 BP.

XX AC AAT31151;

XX DT 12-SEP-1996 (first entry)

XX DE HDV reverse primer HDV17-68.

XX KW Alphavirus; Sindbis virus; vector; gene therapy; vaccine;  
 KW polymerase chain reaction; PCR; primer; hepatitis delta virus; HDV;  
 KW ribozyme; ss.

XX OS Synthetic.

XX PN WO9617072-A2.

XX PD 06-JUN-1996.

XX PF 30-NOV-1995; 95WO-US015490.

XX PR 30-NOV-1994; 94US-00348472.

XX PR 18-JAN-1995; 95US-00376184.

XX PR 15-MAR-1995; 95US-00405827.

XX PA (CHIR ) CHIRON VIAGENE INC.

XX PI Dubensky TW, Polo JM, Ibanez CE, Chang SMW, Jolly DJ, Driver DA;  
 PI Belli BA;

XX DR WPI; 1996-277785/28.

XX PT New recombinant alpha-virus vectors - used to develop prods and methods  
 PT for use in gene therapy and in the prodn. of vaccines.

XX PS Example 7; Page 120; 256pp; English.

XX CC Primer HDV17-68 (AAT31151) is based on hepatitis delta virus (HDV)  
 CC nucleotides 839-887. It was used with reverse primer HDV49-XC (AAT30850)  
 CC for the PCR amplification of HDV sequences. A second primer pair, SIN-HDV  
 CC (AAT31152) and SIN276-SPE (AAT31153), is used to amplify a fragment  
 CC contg. Sindbis 5'-end sequences fused to HDV sequences. Overlapping  
 CC synthesis is used in a second round of PCR using primers HDV49-XC and  
 CC SIN276-SPE. The resulting construct contains the expression cassette  
 CC elements HDV ribozyme/Sindbis 5'-end 299 nts/Sindbis junction  
 CC region/Sindbis structural protein genes/Sindbis 3'-end untranslated  
 CC line cassettes designated pd5'268. This was inserted into pcDNA3. Packaging cell  
 CC structural proteins via alphavirus vectors

XX SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 42.8%; Score 24.4; DB 2; Length 52;  
 Best Local Similarity 59.4%; Pred. No. 33;  
 Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
 Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCGCAUGCG 35  
 :||||:||||:||||:||||:||||:||||:||||:  
 Db 1 TCCACCTCTCGCGGTCGCGACCTGGCATCCG 32

RESULT 11

AAT30817

ID AAT30817 standard; DNA; 52 BP.

XX AC AAT30817;

XX DT 12-SEP-1996 (first entry)

XX DE HDV ribozyme primer HDV17-68.

XX KW Alphavirus; Sindbis virus; vector; gene therapy; vaccine; primer;  
 KW polymerase chain reaction; PCR; ELVIS; ribozyme; HDV;  
 KW hepatitis delta virus; ss.

XX OS Synthetic.

XX PN WO9617072-A2.

XX PD 06-JUN-1996.

XX PF 30-NOV-1995; 95WO-US015490.

XX PR 30-NOV-1994; 94US-00348472.

XX PR 18-JAN-1995; 95US-00376184.

XX PR 15-MAR-1995; 95US-00405827.

XX PA (CHIR ) CHIRON VIAGENE INC.

XX PI Dubensky TW, Polo JM, Ibanez CE, Chang SMW, Jolly DJ, Driver DA;  
 PI Belli BA;

XX DR WPI; 1996-277785/28.

XX PT New recombinant alpha-virus vectors - used to develop prods and methods  
 PT for use in gene therapy and in the prodn. of vaccines.

XX PS Example 3; Page 85; 256pp; English.

XX CC Primer SHDV1F (AAT30816) contains a buffer sequence allowing enzyme  
 CC digestion, a SacI site, and a hepatitis delta virus (HDV) ribozyme  
 CC sequence. It was used with nested primer HDV17-68 (AAT30817) and reverse  
 CC primer SHDV84R (AAT30818) to generate an HDV ribozyme. This antigenomic  
 CC ribozyme can be placed between the polyA tract at the 3' end of a Sindbis  
 CC virus-based eukaryotic layered vector initiation system, ELVIS, and the  
 CC transcription terminal signals to produce alphavirus expression vectors  
 CC useful in methods of gene therapy and for vaccine prodn

XX SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 42.8%; Score 24.4; DB 2; Length 52;  
 Best Local Similarity 59.4%; Pred. No. 33;  
 Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCGCAUGCG 35  
 :||||:||||:||||:||||:||||:||||:||||:  
 Db 1 TCCACCTCTCGCGGTCGCGACCTGGCATCCG 32

RESULT 12

AAV42394

ID AAV42394 standard; DNA; 52 BP.

XX AC AAV42394;

```

XX DT 02-OCT-1998 (first entry)
XX DE Nested PCR primer HDV17-68 of the invention.
XX KW DNA alphavirus; structural protein expression; inhibit; pathogen;
XX KW immune response; stimulate; PCR primer; ss.
XX OS Synthetic.
XX PN US5789245-A.
XX PD 04-AUG-1998.
XX PF 30-OCT-1996; 96US-00741881.
XX PR 15-SEP-1993; 93US-00122791.
XX PR 18-FEB-1994; 94US-00198450.
XX PR 30-NOV-1994; 94US-00348472.
XX PR 20-JAN-1995; 95US-00376184.
XX PR 15-MAR-1995; 95US-00404796.
XX PA (CHIR ) CHIRON CORP.
XX PI Chang SMW, Ibanez CE, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
XX DR WPI; 1998-446089/38.
XX PT DNA alpha:virus structural protein expression cassettes - for producing
XX PT recombinant alpha:virus particles.
XX PS Example 3; Col 69; 140pp; English.
XX CC PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
XX CC invention. The specification describes a DNA alphavirus structural
XX CC protein expression cassette which comprises an inducible promoter and an
XX CC alphavirus structural protein gene, where the promoter directs the
XX CC expression of the alphavirus structural protein gene upon induction of
XX CC the promoter within a cell, and where prior to induction within the cell,
XX CC the expression cassette does not express sufficient quantities of
XX CC structural proteins to be cytotoxic to a BHK cell containing the
XX CC expression cassette. The products may be used to inhibit pathogens and
XX CC stimulate an immune response
XX SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 42.8%; Score 24.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 33;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGUNNNNNUGGCAUGCG 35
   :||||:||||:||||:||||:||||:
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 13
AAV42426
ID AAV42426 standard; DNA; 52 BP.
XX AC AAV42426;
XX DT 02-OCT-1998 (first entry)
XX DE Forward PCR primer HDV17-68.
XX KW DNA alphavirus; structural protein expression; inhibit; pathogen;
XX KW immune response; stimulate; PCR primer; ss.
XX OS Synthetic.
XX PN US5789245-A.
XX PD 04-AUG-1998.

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XX PF 30-OCT-1996; 96US-00741881.
XX PR 15-SEP-1993; 93US-00122791.
XX PR 18-FEB-1994; 94US-00198450.
XX PR 30-NOV-1994; 94US-00348472.
XX PR 20-JAN-1995; 95US-00376184.
XX PR 15-MAR-1995; 95US-00404796.
XX PA (CHIR ) CHIRON CORP.
XX PI Chang SMW, Ibanez CE, Jolly DJ, Dubensky TW, Driver DA, Polo JM;
XX DR WPI; 1998-446089/38.
XX PT DNA alpha:virus structural protein expression cassettes - for producing
XX PT recombinant alpha:virus particles.
XX PS Example 7; Col 103; 140pp; English.
XX CC PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
XX CC invention. The specification describes a DNA alphavirus structural
XX CC protein expression cassette which comprises an inducible promoter and an
XX CC alphavirus structural protein gene, where the promoter directs the
XX CC expression of the alphavirus structural protein gene upon induction of
XX CC the promoter within a cell, and where prior to induction within the cell,
XX CC the expression cassette does not express sufficient quantities of
XX CC structural proteins to be cytotoxic to a BHK cell containing the
XX CC expression cassette. The products may be used to inhibit pathogens and
XX CC stimulate an immune response
XX SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 42.8%; Score 24.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 33;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 4 UCCACCUCCUGCGGUNNNNNUGGCAUGCG 35
   :||||:||||:||||:||||:||||:
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32

RESULT 14
AAV60154
ID AAV60154 standard; DNA; 52 BP.
XX AC AAV60154;
XX DT 25-MAR-2003 (revised)
XX DT 04-DEC-1998 (first entry)
XX DE Nested PCR primer HDV17-68.
XX KW Eukaryotic layered vector initiation system; stimulate; immune response;
XX KW Sindbis; PCR primer; ss.
XX OS Synthetic.
XX OS Hepatitis D virus.
XX PN US5814482-A.
XX PD 29-SEP-1998.
XX PF 30-OCT-1996; 96US-00739158.
XX PR 15-SEP-1993; 93US-00122791.
XX PR 18-FEB-1994; 94US-00198450.
XX PR 14-SEP-1994; 94WO-US010469.
XX PR 30-NOV-1994; 94US-00348472.
XX PR 18-JAN-1995; 95US-00376184.
XX PR 15-MAR-1995; 95US-00404796.
XX PA (POLO/) POLO J M.

```

```
PA (DUBE//) DUBENSKY T W.
PA (JOLLY//) JOLLY D J.
PA (DRIV//) DRIVER D A.
XX
PI Driver DA, Polo JM, Jolly DJ, Dubensky TW;
XX
DR WPI; 1998-541753/46.
XX
PT Eukaryotic layered vector initiation system - containing eukaryotic
PT promoter and heterologous antigen coding sequence, useful for stimulating
PT immune response.
XX
PS Example 3; Col 71-72; 144pp; English.
XX
CC PCR primers AAV60153-55 are used to amplify Hepatitis delta virus
CC ribozyme sequence. The product is used in the course of the invention.
CC The specification describes an eukaryotic layered vector initiation
CC system, based on Sindbis. The eukaryotic layered vector initiation
CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
CC The RNA comprises a vector construct which autonomously amplifies in the
CC cell and expresses a heterologous nucleic acid sequence which encodes an
CC antigen or modified form that stimulates an immune response within an
CC animal. The system is useful for stimulating an immune response to an
CC antigen by introducing the vector into target cells, preferably by
CC infection in vivo, especially where the immune response is a cell
CC mediated, HLA class I-restricted or an HLA class II-restricted immune
CC response. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
XX
Query Match 42.8%; Score 24.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 33;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
Qy 4 UCCACCCUCCGCGGUNNNNNNUGGCGAUGCG 35
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
RESULT 15
AAV60185
ID AAV60185 standard; DNA; 52 BP.
XX
AC AAV60185;
XX
DT 25-MAR-2003 (revised)
DT 04-DEC-1998 (first entry)
XX
DE Reverse PCR primer HDV17-68.
XX
KW Eukaryotic layered vector initiation system; stimulate; immune response;
KW Sindbis; PCR primer; ss.
XX
OS Synthetic.
XX
PN US5814482-A.
XX
PD 29-SEP-1998.
XX
PF 30-OCT-1996; 96US-00739158.
XX
PR 15-SEP-1993; 93US-00122791.
PR 18-FEB-1994; 94US-00198450.
PR 14-SEP-1994; 94WO-US010469.
PR 30-NOV-1994; 94US-00348472.
PR 18-JAN-1995; 95US-00376184.
PR 15-MAR-1995; 95US-00404796.
XX
(POLO//) POLO J M.
PA (DUBE//) DUBENSKY T W.
PA (JOLLY//) JOLLY D J.
PA (DRIV//) DRIVER D A.
```

```
XX
PI Driver DA, Polo JM, Jolly DJ, Dubensky TW;
XX
DR WPI; 1998-541753/46.
XX
PT Eukaryotic layered vector initiation system - containing eukaryotic
PT promoter and heterologous antigen coding sequence, useful for stimulating
PT immune response.
XX
PS Example 5; Col 108; 144pp; English.
XX
CC PCR primers AAV60184-85 are used in the course of the invention. The
CC specification describes an eukaryotic layered vector initiation system,
CC based on Sindbis. The eukaryotic layered vector initiation system
CC comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a
CC susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA.
CC The RNA comprises a vector construct which autonomously amplifies in the
CC cell and expresses a heterologous nucleic acid sequence which encodes an
CC antigen or modified form that stimulates an immune response within an
CC animal. The system is useful for stimulating an immune response to an
CC antigen by introducing the vector into target cells, preferably by
CC infection in vivo, especially where the immune response is a cell
CC mediated, HLA class I-restricted or an HLA class II-restricted immune
CC response. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
XX
Query Match 42.8%; Score 24.4; DB 2; Length 52;
Best Local Similarity 59.4%; Pred. No. 33;
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
Qy 4 UCCACCCUCCGCGGUNNNNNNUGGCGAUGCG 35
Db 1 TCCACCTCTCGCGGTCCGACCTGGGCATCCG 32
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Search completed: October 29, 2005, 08:21:09  
Job time : 455 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 29, 2005, 02:35:43 ; Search time 2993 Seconds  
(without alignments)  
724.913 Million cell updates/sec

Title: US-09-699-667E-61

Perfect score: 57  
Sequence: 1 ggguccaccuccgagggun.....uuecgauagggaagccac 57

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0  
Maximum DB seq length: 150

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	42.1	123	1	AU077016
C 2	21.6	37.9	129	8	AZ937579 2M0195L18
C 3	21.2	37.2	141	4	BT007258
C 4	21.2	37.2	147	1	AA094039
C 5	21	36.8	148	2	BF368659
C 6	20.6	36.1	114	1	AV848738
C 7	20.6	36.1	117	9	BX907242
C 8	20.6	36.1	117	9	LBAP063G06
C 9	20.6	36.1	118	1	AV855799
C 10	20.6	36.1	135	8	CC043330
C 11	20.2	35.4	109	2	BF875943
C 12	20.2	35.4	118	2	BE595364
C 13	20.2	35.4	125	1	AA856004
C 14	20.2	35.4	144	6	CD863940
C 15	20.2	35.4	147	6	CD863940
C 16	20	35.1	137	1	AA207969
C 17	20	35.1	143	8	AZ407850
C 18	19.8	34.7	61	7	CH482613
C 19	19.8	34.7	105	8	BH215680
C 20	19.8	34.7	108	2	AW401242
C 21	19.8	34.7	135	7	CQ989014
C 22	19.8	34.7	145	8	BZ199525
C 23	19.6	34.4	112	4	BM286935
C 24	19.6	34.4	119	8	BH173238

C 25	19.6	34.4	123	4	BG693687
C 26	19.6	34.4	136	8	BH035997
C 27	19.6	34.4	140	8	CC019353
C 28	19.6	34.4	146	4	BM746675
C 29	19.4	34.0	49	1	AI956143
C 30	19.4	34.0	117	4	BI021544
C 31	19.4	34.0	137	4	BI026587
C 32	19.4	34.0	147	2	BF788210
C 33	19.4	34.0	150	8	BH220875
C 34	19.2	33.7	110	4	BM100180
C 35	19.2	33.7	116	4	BM029915
C 36	19	33.3	111	7	CO788089
C 37	19	33.3	120	1	AI153878
C 38	19	33.3	129	1	AA471148
C 39	19	33.3	136	8	BH616926
C 40	19	33.3	140	1	AV847196
C 41	19	33.3	148	2	BB482390
C 42	19	33.3	149	2	BE362950
C 43	18.8	33.0	73	4	EG035546
C 44	18.8	33.0	85	6	CD036231
C 45	18.8	33.0	90	8	AZ307919

## ALIGNMENTS

RESULT 1  
AU077016/c  
LOCUS AU077016 123 bp mRNA linear EST 04-MAY-2000  
DEFINITION AU077016 Sugano cDNA library Homo sapiens cDNA clone Rp-A0037 similar to 5'-end region of Human aminoacylase-1 (ACV1) mRNA, mRNA sequence.

ACCESSION AU077016  
VERSION AU077016.1 GI:7439584

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 123)

AUTHORS Suzuki, Y., Ishihara, D., Sasaki, M., Nakagawa, H., Hata, H., Tsunoda, T., Watanabe, M., Komatsu, T., Oka, T., Isogai, T., Suyama, A.

TITLE Statistical analysis of the 5' untranslated region of human mRNA using 'Oligo-Capped' cDNA libraries

JOURNAL Genomics 64 (3), 286-297 (2000)

MEDLINE 20221373

PUBMED 10756096

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997)

This clone was obtained from a 'full length-enriched' cDNA library constructed by 'Oligo-Capping' method. The coding region starts from the 50 bp upstream to the 3'-end.

FEATURES

source

1..123

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="Rp-A0037"

/clone\_lib="Sugano cDNA library"

ORIGIN

Query Match 42.1%; Score 24; DB 1; Length 123;

Best Local Similarity 50.0%; Pred. No. 5.8e+02;

Matches 23; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

Qy 1 GGGUCCACCUCCGCGGNNNNNNNUGGCGAUGCGGCUUGCGAUGG 46  
 Db 105 GGGTCTCTCTCGGACCTTCTGTCATGCGTGGCGCGG 60

RESULT 2  
 AZ937579/c  
 LOCUS 129 bp DNA linear GSS 26-APR-2001  
 DEFINITION 2M0195L18R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0195L18 R, genomic survey sequence.

ACCESSION AZ937579  
 VERSION AZ937579.1 GI:13796530  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 129)  
 Dunn, B., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.,  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0195 row: L column: 18

Seq primer: CACACGAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 129.

Location/Qualifiers

FEATURES

source

1..129

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0195L18"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match

Best Local Similarity 37.9%; Score 21.6; DB 8; Length 129;

Matches 23; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 4 UCCACCUCCGCGGNNNNNNNUGGCGAUGCGGCUUGCGAUGG 53  
 Db 112 TCCTCTCTCTTGGGAATCCCGGGCCTCTGCTTCTTGTGCAAG 63

RESULT 3  
 BI007258/c

LOCUS

DEFINITION BI007258 141 bp mRNA linear EST 13-JUN-2001

ACCESSION MR1-RT0079-220101-011-e07 RT0079 Homo sapiens cDNA, mRNA sequence.

VERSION BI007258

KEYWORDS BI007258.1 GI:14411329

SOURCE EST.

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 141)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR1&t2=MR1-RT0079-

220101-011-e07&t3=2001-01-22&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 46

High quality sequence stop: 122.

Location/Qualifiers

FEATURES

source

1..141

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="RT0079"

/notes="Organ: kidney tumor; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match

Best Local Similarity 37.2%; Score 21.2; DB 4; Length 141;

Matches 21; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

10 UCCUGCGGNNNNNUGGCGGCUUGCGAUGCGCUAAGGACCCC 57

98 TTCTCCATGTTGATGGTGGGATGCTGTTCCGGAGTAATAGGTACCC 51

RESULT 4

RA094039/c

LOCUS

DEFINITION

AA094039

cl1641.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens

cDNA 5', mRNA sequence.

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ACCESSION AA094039          37.2%; Score 21.2; DB 1; Length 147;
VERSION    AA094039.1      52.1%; Pred. No. 5.6e+03;
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE      1 (bases 1 to 147)
JOURNAL    cDNAs from fetal heart (1996)
COMMENT    Unpublished (1996)
           Contact: Liow CC
           Brigham and Women's Hospital
           Harvard Medical School
           75 Francis St. Boston, MA 02115, USA
           Tel: 6177328915
           Fax: 6179750995
           Email: cliow@rics.bwh.harvard.edu
           PCR Primers
FORWARD: 5' GCCAAGCTCGAAATTAACCTCACTAAAGG 3'
BACKWARD: 5' CCAAGTGAATTTGAATCACTCACTATAGGCG 3'
Seq primer: 5' GAAATTAACCTCACTAAAGG 3'
FEATURES   Location/Qualifiers
           source          1..147
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /lab_hosts="E. coli XL1-Blue"
           /clone_lib="Human fetal heart, Lambda ZAP Express"
           /notes="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
           XhoI; mRNA was purified from human fetal hearts (8-10
           weeks). cDNA was synthesized using a XhoI-Oligo dT
           adaptor-primer. EcoRI adaptors were ligated, followed by
           digestion with XhoI, for directional cloning into
           predigested lambda ZAP Express."
ORIGIN
Query Match          37.2%; Score 21.2; DB 1; Length 147;
Best Local Similarity 52.1%; Pred. No. 5.6e+03;
Matches 25; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy  7 ACCUCCUGCGGNNNNNUGGCAUGCGGCUUGCAUGGCUAAGGGA 54
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  115 ACCTCTCGCGATTTTGACTGTCGACATCCGCGGCTCATGCCAATAGGA 68

RESULT 5
BF368659/c          148 bp mRNA linear EST 24-NOV-2000
LOCUS              QV1-GN0063-290800-347-c02_1 GN0063 Homo sapiens cDNA, mRNA
DEFINITION          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS             Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE               1 (bases 1 to 148)
JOURNAL             Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
COMMENT             Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
                   Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
                   Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
                   O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                   Simpson, A.J.
                   Shotgun sequencing of the human transcriptome with ORF expressed
                   sequence tags
JOURNAL             Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE             20202663
PUBMED              10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research

```

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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-GN0063-
290800-347-c02_1&t3=2000-08-29&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 148.
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           source          1..148
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /dev_stage="Adult"
           /clone_lib="GN0063"
           /notes="Organ: placenta normal; Vector: puc18; Site_1:
           SmaI; Site_2: SmaI; A mini-library was made by cloning
           products derived from ORESTES PCR (U.S. Letters Patent
           application No. 196,716 - Ludwig Institute for Cancer
           Research) profiles into the puc 18 vector. Reverse
           transcription of tissue mRNA and cDNA amplification were
           performed under low stringency conditions."
ORIGIN
Query Match          36.8%; Score 21; DB 2; Length 148;
Best Local Similarity 43.1%; Pred. No. 6.5e+03;
Matches 22; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy  3 GUCCACUCCUCCGCGNNNNNUGGCAUGCGGCUUGCAUGGCUAAGG 53
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  137 GTCACCTCCAGGTGTGTTCTCTGAAGATGCTTGACTATGCTAAGAG 87

RESULT 6
AV848738/c          114 bp mRNA linear EST 08-NOV-2001
LOCUS              AV848738 Nori Satoh unpublished cDNA library, young adult Ciona
DEFINITION          intestinalis cDNA clone rcia14f13 3', mRNA sequence.
AUTHORS             Ciona intestinalis
TITLE               Ciona intestinalis
JOURNAL             Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
COMMENT             1 (bases 1 to 114)
                   Satoh, N., Satoh, Y., Kohara, Y. and Shin-i, T.
                   Expressed genes in Ciona intestinalis
                   Unpublished (2000)
                   Contact: Nori Satoh
                   Department of Zoology
                   Kyoto University
                   Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
                   Tel: 81-75-753-4081
                   Fax: 81-75-705-1113
                   Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES   Location/Qualifiers
           source          1..114
           /organism="Ciona intestinalis"
           /mol_type="mRNA"
           /db_xref="taxon:7719"
           /clone_lib="rcia14f13"
           /tissue_type="whole animal"
           /dev_stage="young adult"
           /clone_lib="Nori Satoh unpublished cDNA library, young
           adult"
ORIGIN
Query Match          36.1%; Score 20.6; DB 1; Length 114;
Best Local Similarity 48.5%; Pred. No. 8.9e+03;

```

```

Matches 16; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 13 UCGCGGNNNNNUGGCGAUGCGGCUUCGCAUG 45
      :||||:      :|:|||||:|:|:|:|:|:|:|
Db 106 TCGCGTGGCTGCTGCACCTGGCGGCTTCGGATG 74

RESULT 7
LOCUS BX907242 117 bp DNA linear GSS 07-JAN-2004
DEFINITION Leishmania braziliensis GSS, clone LBAF063G06, genomic survey
sequence.
ACCESSION BX907242
VERSION BX907242.1 GI:40735710
KEYWORDS GSS; genomic survey sequence.
SOURCE Leishmania braziliensis
ORGANISM Leishmania braziliensis
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania; Leishmania braziliensis species complex.
REFERENCE 1
AUTHORS Laurentino,E.C., Ruiz,J.C. and Cruz,A.K.
TITLE GSS analysis of the Leishmania braziliensis genome
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 117)
SOURCE Cruz,A.K.
COMMENT Direct Submission
TITLE Submitted (07-JAN-2004) Cruz A.K., University of Sao Paulo,
JOURNAL Department of Molecular and Cell Biology, FMRP, Avenida
Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL
Clone requests: akcruze@fmrp.usp.br.
FEATURES
source
1..117
Location/Qualifiers
/organism="Leishmania braziliensis"
/mol_type="genomic DNA"
/strain="WHOM/BR/75/M2904"
/db_xref="taxon:5660"
/clone="LBAF063G06"

ORIGIN
Query Match 36.1%; Score 20.6; DB 9; Length 117;
Best Local Similarity 47.4%; Pred. No. 8.9e+03;
Matches 27; Conservative 5; Mismatches 25; Indels 0; Gaps 0;

Qy 1 GGGUCCACUCCUGCGGNNNNNUGGCGAUGCGGCUUCGCAUGGAGGACCC 57
      :||||:      :|:|||||:|:|:|:|:|:|:|
Db 47 GCGCCACTATCTCGGTCTCCACCTGGGCGATCCCTCGGGATGTCGGAGGCACC 103

RESULT 8
LOCUS LBAF063G06 117 bp DNA linear GSS 20-JUN-2003
DEFINITION Leishmania braziliensis GSS, clone LBAF063G06, genomic survey
sequence.
ACCESSION BX543887
VERSION BX543887.1 GI:32138222
KEYWORDS GSS; genomic survey sequence.
SOURCE Leishmania braziliensis
ORGANISM Leishmania braziliensis
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania; Leishmania braziliensis species complex.
REFERENCE 1
AUTHORS Laurentino,E.C., Ruiz,J.C. and Cruz,A.K.
TITLE GSS analysis of the Leishmania braziliensis genome
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 117)
SOURCE Cruz,A.K.
COMMENT Direct Submission
TITLE Submitted (17-JUN-2003) Cruz A.K., University of Sao Paulo,
JOURNAL Department of Molecular and Cell Biology, FMRP, Avenida
Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL
Clone requests: akcruze@fmrp.usp.br.
FEATURES
source
1..117
Location/Qualifiers
/organism="Leishmania braziliensis"
/mol_type="genomic DNA"
/strain="WHOM/BR/75/M2904"
/db_xref="taxon:5660"
/clone="LBAF063G06"

ORIGIN
Query Match 36.1%; Score 20.6; DB 9; Length 117;
Best Local Similarity 47.4%; Pred. No. 8.9e+03;
Matches 27; Conservative 5; Mismatches 25; Indels 0; Gaps 0;

Qy 1 GGGUCCACUCCUGCGGNNNNNUGGCGAUGCGGCUUCGCAUGGAGGACCC 57
      :||||:      :|:|||||:|:|:|:|:|:|:|
Db 47 GCGCCACTATCTCGGTCTCCACCTGGGCGATCCCTCGGGATGTCGGAGGCACC 103

RESULT 9
LOCUS AV855799 118 bp mRNA linear EST 08-NOV-2001
DEFINITION AV855799 Nori Satoh unpublished cDNA library, egg Ciona
intestinalis cDNA clone rcieg19m19 3', mRNA sequence.
ACCESSION AV855799
VERSION AV855799.1 GI:16843323
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 118)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES
source
1..118
Location/Qualifiers
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcieg19m19"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN
Query Match 36.1%; Score 20.6; DB 1; Length 118;
Best Local Similarity 48.5%; Pred. No. 8.9e+03;
Matches 16; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 13 UCGCGGNNNNNUGGCGAUGCGGCUUCGCAUG 45
      :||||:      :|:|||||:|:|:|:|:|:|:|
Db 110 TCGCGTGGCTGCTGCACCTGGCGGCTTCGGATG 78

RESULT 10
LOCUS CC043330 135 bp DNA linear GSS 01-APR-2003
DEFINITION 3591_1_157_1_H10.Y.1 3591 - RescueMu Grid P Zea mays genomic,
genomic survey sequence.
ACCESSION CC043330
VERSION CC043330.1 GI:29458221
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 135)

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/organism="Leishmania braziliensis"
/mol_type="genomic DNA"
/strain="WHOM/BR/75/M2904"
/db_xref="taxon:5660"
/clone="LBAF063G06"

ORIGIN
Query Match 36.1%; Score 20.6; DB 9; Length 117;
Best Local Similarity 47.4%; Pred. No. 8.9e+03;
Matches 27; Conservative 5; Mismatches 25; Indels 0; Gaps 0;

Qy 1 GGGUCCACUCCUGCGGNNNNNUGGCGAUGCGGCUUCGCAUGGAGGACCC 57
      :||||:      :|:|||||:|:~|:|:|:|:|:|:|
Db 47 GCGCCACTATCTCGGTCTCCACCTGGGCGATCCCTCGGGATGTCGGAGGCACC 103

RESULT 9
LOCUS AV855799 118 bp mRNA linear EST 08-NOV-2001
DEFINITION AV855799 Nori Satoh unpublished cDNA library, egg Ciona
intestinalis cDNA clone rcieg19m19 3', mRNA sequence.
ACCESSION AV855799
VERSION AV855799.1 GI:16843323
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 118)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES
source
1..118
Location/Qualifiers
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcieg19m19"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN
Query Match 36.1%; Score 20.6; DB 1; Length 118;
Best Local Similarity 48.5%; Pred. No. 8.9e+03;
Matches 16; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 13 UCGCGGNNNNNUGGCGAUGCGGCUUCGCAUG 45
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Db 110 TCGCGTGGCTGCTGCACCTGGCGGCTTCGGATG 78

RESULT 10
LOCUS CC043330 135 bp DNA linear GSS 01-APR-2003
DEFINITION 3591_1_157_1_H10.Y.1 3591 - RescueMu Grid P Zea mays genomic,
genomic survey sequence.
ACCESSION CC043330
VERSION CC043330.1 GI:29458221
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 135)

```



**AUTHORS** Walbot, V.  
**TITLE** Maize genomic sequences found using engineered RescueMu transposon  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2247  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Possible ligation site so sequence was trimmed. Post-ligation  
 sequence submitted separately.  
 Plate: 3591\_1\_157\_1 row: 29  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1. 135  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultivar="mixed background W23/A188/B73/K55"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="3591 - RescueMu Grid P"  
 /note="Organ: leaf; Vector: RescueMu (engineered from  
 pBluescript backbone); Site\_1: BamHI; Site\_2: BglII;  
 RescueMu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on RescueMu, go to the web  
 site 'www.zmdb.iastate.edu' and follow the links for  
 'RescueMu.' Grid P was grown at Molokai in 2002. DNA was  
 extracted from leaf strips, double digested using BamHI  
 and BglII, and ligated to form circular plasmids. DH10B  
 cells were transformed and then screened on LB plates with  
 ampicillin."

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ORIGIN
Query Match 36.1%; Score 20.6; DB 8; Length 135;
Best Local Similarity 46.9%; Pred. No. 9e+03;
Matches 23; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 9 CUCUCGCGGNNNNNUGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
   ||| ||| :||| ||| ||| ||| ||| ||| |||
Db 15 CTGCTGCTGTCGTGATGACACGGCGGATTCGCAGTGGCATGCACAC 63

RESULT 11
BF875943
LOCUS
DEFINITION CM0-ET0163-111100-687-g07 ET0163 Homo sapiens cDNA, mRNA sequence.
VERSION BF875943
ACCESSION BF875943.1 GI:12266073
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 109)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matcukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
COMMENT

```

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-ET0163-111100-687-g07&t3=2000-11-11&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 109.  
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1. .109  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="ET0163"  
/notes="Organ: lung\_tumor; Vector: puc18; Site: 1: SmaI;  
Site: 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

ORIGIN  
Query Match 35.4%; Score 20.2; DB 2; Length 109;  
Best Local Similarity 53.8%; Pred. No. 1.2e+04;  
Matches 21; Conservative 4; Mismatches 14; Indels 0; Gaps 0;  
  
Qy 14 CGCGGUNNNNUGGCAUGCGGUUCGCAUGGCUAAGG 52  
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Db 9 CGCGGTCTTACTGCGAAGGCGGCTTCTTACTGCGAAGG 47  
  
RESULT 12  
BE595364/c  
LOCUS  
DEFINITION  
P11\_53\_C03\_b1\_A002 Pathogen induced 1 (P11) Sorghum bicolor cDNA,  
mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Sorghum bicolor (sorghum)  
Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 118)  
Cordonnier-Pratt,M.-M., Gingle,A., Dean,R., Sudman,M. and  
Pratt,L.H.  
An EST database from Sorghum: pathogen-induced plants  
Unpublished (2000)  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions  
below Phred quality 16. The threshold for highest quality sequence  
is 20.  
Seq primer: JEN REV  
High quality sequence stop: 100  
POLYA=No.  
Location/Qualifiers  
1. .118  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/db\_xref="taxon:4558"  
/clone\_lib="Pathogen induced 1 (P11)"

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/dev\_stage="Adult"  
/clone\_lib="ET0163"  
/notes="Organ: lung\_tumor; Vector: puc18; Site: 1: SmaI;  
Site: 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."



```

Pooideae; Triticeae; Triticum.
1 (bases 1 to 147)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr).
location/Qualifiers
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/organism="Triticum aestivum"
/mol_type="mRNA"
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/clone="AZO1108J17"
/tissue_type="leaf"
/clone_lib="AZO1"

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source
35.4%; Score 20.2; DB 6; Length 147;
Query Match
Best Local Similarity 45.5%; Pred. No. 1.2e+04;
Matches 25; Conservative 6; Mismatches 24; Indels 0; Gaps

QY 3 GUCCACCCUCCGCGGUNNNNNUGGCAUGCGCGUUCGCAUGGCUAAGGAGCC 57
Db 25 GTGCTCTCCAGGCGCGCGCGTCCGCGCGTCCGCGTGGCGAACCGGCC 79

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Search completed: October 29, 2005, 09:39:59  
Job time : 3002 secs

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 45 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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1. .57
Location/Qualifiers
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/db_xref="taxon:32630"
/notes="synthetic nucleic acid"
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Best Local Similarity 71.9%; Pred. No. 4.5e-06;
Matches 41; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GGGUCCACUCCUGCGGUNNNNNUGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
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Db 1 GGGTCCACCTCTCGGGTCCGCTGGGCATGGGCTTCGCATGGCTAAGGGACCC 57
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RESULT 3
AX012285 57 bp RNA linear PAT 06-SEP-2000
LOCUS
DEFINITION
Sequence 47 from Patent WO9955856.
ACCESSION
AX012285
VERSION
AX012285.1 GI:9998346
KEYWORDS
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 47 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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/db_xref="taxon:32630"
/notes="synthetic nucleic acid"
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Query Match 89.5%; Score 51; DB 6; Length 57;
Best Local Similarity 71.9%; Pred. No. 4.5e-06;
Matches 41; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GGGUCCACUCCUGCGGUNNNNNUGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
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Db 1 GGGTCCACCTCTCGGGTCCGCTGGGCATGGGCTTCGCATGGCTAAGGGACCC 57
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 4
AX012286 57 bp RNA linear PAT 06-SEP-2000
LOCUS
DEFINITION
Sequence 48 from Patent WO9955856.
ACCESSION
AX012286
VERSION
AX012286.1 GI:9998347
KEYWORDS
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 48 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
other sequences; artificial sequences.
1
REFERENCE
AUTHORS
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 49 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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/db_xref="taxon:32630"
/notes="synthetic nucleic acid"
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Query Match 89.5%; Score 51; DB 6; Length 57;
Best Local Similarity 71.9%; Pred. No. 4.5e-06;
Matches 41; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GGGUCCACUCCUGCGGUNNNNNUGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 5
AX012287 57 bp RNA linear PAT 06-SEP-2000
LOCUS
DEFINITION
Sequence 49 from Patent WO9955856.
ACCESSION
AX012287
VERSION
AX012287.1 GI:9998348
KEYWORDS
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 49 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="synthetic nucleic acid"
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Best Local Similarity 71.9%; Pred. No. 4.5e-06;
Matches 41; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GGGUCCACUCCUGCGGUNNNNNUGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
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Db 1 GGGTCCACCTCTCGGGTCCGCTGGGCATGGGCTTCGCATGGCTAAGGGACCC 57
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 6
AX012288 57 bp RNA linear PAT 06-SEP-2000
LOCUS
DEFINITION
Sequence 50 from Patent WO9955856.
ACCESSION
AX012288
VERSION
AX012288.1 GI:9998349
KEYWORDS
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
ANANVRANICH S., Lafontaine,D. and Perreault,J.P.
TITLE
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 50 04-NOV-1999;
ANANVRANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
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1. .57
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Db 1 GGGTCCACCTCTCGGGTCCGATCTGGGCATCGCGCTTCGCATGGCTAAGGGACCC 57

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ACCESSION AX012284  
VERSION AX012284.1 GI:9998345  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.  
TITLE Nucleic acid enzyme for rna cleavage  
JOURNAL Patent: WO 9955856-A 46 04-NOV-1999;  
ANANVORANICH SRINIVART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN  
PIERRE (CA); UNIV SHERBROOKE (CA)  
FEATURES  
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/note="synthetic nucleic acid"

ORIGIN  
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Matches 37; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GGGUCCACUCCUCCGGGUNNNNUGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57  
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Db 1 GGGTCCACCTCTCGGGTCCGATCTGGGCATCGCGCTTCGCATGGCTAAGGGACCC 57

RESULT 10  
AX012291  
LOCUS AX012291  
DEFINITION Sequence 53 from Patent WO9955856.  
ACCESSION AX012291  
VERSION AX012291.1 GI:9998352  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Ananvoranich,S., Lafontaine,D. and Perreault,J.P.  
TITLE Nucleic acid enzyme for rna cleavage  
JOURNAL Patent: WO 9955856-A 53 04-NOV-1999;  
ANANVORANICH SRINIVART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN  
PIERRE (CA); UNIV SHERBROOKE (CA)  
FEATURES  
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/db\_xref="taxon:32630"  
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Best Local Similarity 67.6%; Pred. No. 14;  
Matches 25; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGUCCACUCCUCCGGGUNNNNUGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 37  
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Db 1 GGGTCCACCTCTCGGGTCCGATCTGGGCATCGCGCTTCGCATGGCTAAGGGACCC 37

RESULT 11  
141390  
LOCUS 141390  
DEFINITION Sequence 18 from patent US 5625047.  
LOCUS 141390  
linear PAT 13-MAY-1997

ACCESSION I41390  
VERSION I41390.1 GI:2081980  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 61)  
AUTHORS Been,M.D., Rosenstein,S.P. and Perrotta,A.T.  
TITLE Enzymatic RNA molecules  
JOURNAL Patent: US 5625047-A 18 29-APR-1997;  
FEATURES Location/Qualifiers  
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1. .61  
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Best Local Similarity 58.5%; Pred. No. 6.3e+02;  
Matches 31; Conservative 10; Mismatches 8; Indels 4; Gaps 1;  
Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCAUGCGGCUAGGACG 56  
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Db 8 TCCACCTCTCGCGTCCGACCTGGGCAT-----CTTCGATGGCTAAGGGAGC 56

RESULT 12  
AR021007  
LOCUS AR021007 52 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 40 from patent US 5789245.  
ACCESSION AR021007  
VERSION AR021007.1 GI:3975622  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W., Jolly,D.J. and Driver,D.A.  
TITLE Alphavirus structural protein expression cassettes  
JOURNAL Patent: US 5789245-A 40 04-AUG-1998;  
FEATURES Location/Qualifiers  
source  
1. .52  
/organism="unknown"  
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ORIGIN  
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Best Local Similarity 59.4%; Pred. No. 1.8e+03;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCAUGCG 35  
:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCG 32

RESULT 13  
AR021047  
LOCUS AR021047 52 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 80 from patent US 5789245.  
ACCESSION AR021047  
VERSION AR021047.1 GI:3975662  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W., Jolly,D.J. and Driver,D.A.  
TITLE Alphavirus structural protein expression cassettes  
JOURNAL Patent: US 5789245-A 80 04-AUG-1998;  
FEATURES Location/Qualifiers  
source  
1. .52  
/organism="unknown"

ORIGIN  
Query Match 42.8%; Score 24.4; DB 6; Length 52;  
Best Local Similarity 59.4%; Pred. No. 1.8e+03;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCAUGCG 35  
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Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCG 32

RESULT 14  
AR043422  
LOCUS AR043422 52 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 40 from patent US 5814482.  
ACCESSION AR043422  
VERSION AR043422.1 GI:5964430  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.  
TITLE Eukaryotic layered vector initiation systems  
JOURNAL Patent: US 5814482-A 40 29-SEP-1998;  
FEATURES Location/Qualifiers  
source  
1. .52  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 42.8%; Score 24.4; DB 6; Length 52;  
Best Local Similarity 59.4%; Pred. No. 1.8e+03;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCAUGCG 35  
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Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCG 32

RESULT 15  
AR043462  
LOCUS AR043462 52 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 80 from patent US 5814482.  
ACCESSION AR043462  
VERSION AR043462.1 GI:5964470  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.  
TITLE Eukaryotic layered vector initiation systems  
JOURNAL Patent: US 5814482-A 80 29-SEP-1998;  
FEATURES Location/Qualifiers  
source  
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ORIGIN  
Query Match 42.8%; Score 24.4; DB 6; Length 52;  
Best Local Similarity 59.4%; Pred. No. 1.8e+03;  
Matches 19; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
Qy 4 UCCACCUCCUGCGGUNNNNNNUGGCAUGCG 35  
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Db 1 TCCACCTCTCGCGTCCGACCTGGGCATCG 32

Search completed: October 29, 2005, 08:49:48  
Job time : 1711 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 29, 2005, 08:12:41 ; Search time 3876 Seconds

(without alignments)

600.339 Million cell updates/sec

Title: US-09-699-667E-61

Perfect score: 57

Sequence: 1 ggguccaccucccgcggun.....uucgauggcuaggagccc 57

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 41414866

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 29, 2005, 08:21:20 ; Search time 1990 Seconds  
(without alignments)  
411.830 Million cell updates/sec

Title: US-09-699-667E-61  
Perfect score: 57  
Sequence: 1 gguccaccuccguggun.....uucgcauggcuaggagccc 57

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27723106 seqs, 7188968421 residues

Total number of hits satisfying chosen parameters: 40003802

Minimum DB seq length: 0  
Maximum DB seq length: 150

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
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